Meta-Genesis. Towards a Biology Without Matter

From Boolean Algebra to the Expansion of Life:
Binary Arithmetic and Multi-Dimensional Projections of the Genetic Code

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Keywords: Boolean algebra, binary arithmetic, genetic code, multi-scale invariants, multi-dimensional projection, biological Bloch sphere, combinatorial expansion of life, mirror symmetry, mathematical genetics, biology without matter, cosmology of information, theory of biological coherence, fractal geometry of life, logical continuum of the code.

Abstract:
This section of *Meta-Genesis* (see references: complete primary data and computational materials at the end of the document), entitled *"From Boolean Algebra to the Expansion of Life: Binary Arithmetic and Multi-Dimensional Projections of the Genetic Code,"* explores the logical structure underlying the code of life based on the foundations of Boolean algebra and binary arithmetic. The genetic code, defined by four bases organized in triplets, is described as a six-dimensional Boolean hypercube (2^6 = 64 states), whose spherical projection helps reveal stable numerical invariants (1, 96–97, 128) identified in the first part (*Multi-Scale Numerical Invariants and Fractal Properties of the Genetic Code: A Combinatorial and Atomic Analysis.* Zenodo. Direct link: https://doi.org/10.5281/zenodo.17068705). These invariants act as organizational constants, ensuring systemic coherence across hierarchical levels — from bases to amino acids, proteins, and genes.

The cubing of the code,

$$f(n) = \frac{n^3}{4}, \quad (TCAG)^3$$

appears as the condition for the logical completeness of the biological system. It allows the three positions of the codon to be represented as the three axes of a complete Boolean space, linking binary logic to the three-dimensional geometry of life. This cubic structure, uniquely capable of encompassing all possible combinations, constitutes the point of origin for the spherical projection and the multi-scale invariants; it acts as the mathematical seed of the combinatorial expansion of life.

The study shows that life does not emerge from pre-existing matter, but from a self-coherent logical structure projected into different geometrical spaces. Binary arithmetic acts as the driving force behind this unfolding, leading to a hierarchy of logical states analogous to those of the Bloch sphere in quantum mechanics. This unfolding is interpreted as an informational expansion comparable to that of the physical universe: a finite system of Boolean rules generating an infinite continuum of coherent states. Thus, biology appears as an internal cosmology of information, where each organism represents a localized projection of a universal invariant code — the true logical field of life.

For this section, the reference book *Binary Arithmetic and Boolean Algebra* by **Angelo C. Gillie** (Professor of Electrical Technology and Chair at Niagara County Community College, New York) was used. This book, which trained several generations of engineers and technicians in the Anglo-Saxon world, remains a key reference in the field.

Methodological Validation Note
Confirmation of the Model through the Cubing of the Genetic Code

The *Mathematical Lens Method*, introduced in the first part of *Meta-Genesis*, proposed linking the atomic properties of the genetic code to quantifiable logical states according to the following relation:

$$v_i = p_i \cdot n_i \cdot e_i$$

where v_i represents the logical value of a codon, p_i the number of protons, n_i the number of neutrons, and eie_iei the number of electrons associated with the principal atoms of life (C, H, O, N).

The corresponding cubic function is:

$$f(n) = \frac{n^3}{4}$$

described a quaternary normalization of the system, based on the presence of four bases, four dominant atoms, and four fundamental logical states.

The present study confirms that this relationship finds its direct justification in the cubing of the genetic code $(TCAG)^3$

The codon triplet, equivalent to three logical degrees of freedom, corresponds to the cubing of a quaternary alphabet. The normalization factor of four reflects the intrinsic quaternary structure of the system, ensuring coherence across the atomic, codonic, and combinatorial levels.

Thus, the function:

$$f(n) = \frac{n^3}{4}$$

is not an empirical approximation, but a canonical expression of the combinatorial behavior of the genetic code. It formalizes the transition from the atomic level (protons, neutrons, electrons) to the logical level of the code, where each codon acts as a cubed Boolean unit — a three-dimensional information cell within a finite natural automaton.

The validation of this equation $(TCAG)^3$ through structural analysis confirms that DNA follows a model of complete logical symmetry, in which the cubing of the code corresponds to the condition of mathematical and geometrical completeness of living systems.

Related Work and Originality of the Proposed Framework

The logical and combinatorial structure of the genetic code has been explored by several authors since the mid-20th century, notably through binary representations and symmetry analyses. The first mathematical treatments, proposed by Yury Rumer (1966), identified an internal bisection symmetry within the standard genetic code, dividing the 64 codons into complementary subsets. Later studies, notably those of Lenstra (2015), formalized this structure using graph theory, Hamming distances, and symmetry groups, demonstrating that the genetic code behaves as a highly ordered combinatorial system embedded in a six-dimensional hypercube (2^6 = 64 states).

The developments of Sánchez et al. (2004, 2005) introduced Boolean lattice models, describing the code as a partially ordered set of binary attributes (purine/pyrimidine, number of hydrogen bonds, etc.). These models show that certain biochemical regularities can emerge from purely logical constraints. In parallel, Nemzer (2016–2017) proposed a binary encoding of the genetic code, assigning two bits to each base (A, C, G, U), thereby producing a six-bit representation for each codon and establishing correlations between bit positions and the physicochemical properties of the corresponding amino acids.

Although these studies have successfully linked Boolean logic to molecular genetics, they remain limited to intra-level descriptions of the canonical 64-codon system. They generally focus on static properties (symmetry, redundancy, degeneracy) within the standard code, without extending this logic to higher levels of biological organization.

The present work extends this framework in three main directions:

1. Multi-scale numerical invariants (1, 96–97, 128) and the constant Δ = 225.5

The analysis introduces invariant numerical patterns that remain constant across several hierarchical levels of living systems — from atomic composition (elements C, H, O, N) and nucleotide doublets (Crick's hypothetical pre-code), to triplets, quaternary expansions, amino acids, and viral coding systems. No previous study has formulated a unified and transversal invariant framework spanning these different biological scales.

2. Structural Inversion (Mirror-Twin Principle)

A new class of transformations is proposed, based on logical inversion rather than chemical complementarity, to explain the recurrent mirror symmetries and phase inversions observed across biological and informational hierarchies.

3. Universal Logical Skeleton

The model generalizes the Boolean structure beyond biology, treating logical tables 2^n (4, 8, 16, 32, 64 states) as a matter-independent logical substrate upon which genetic alphabets can be projected. The genetic code is thus conceived as a particular instance of a universal informational architecture, constrained by the combinatorial limits of binary systems.

In summary, while previous works have sought to *map* the genetic code within Boolean structures, the present study derives biological organization directly from the intrinsic logic of binary combinatorics. This reversal of perspective — from *descriptive* to *generative* — constitutes the main conceptual originality of the proposed framework.

Parallels with Binary Code and Boolean Algebra

In the first paper (*Multi-Scale Numerical Invariants and Fractal Properties of the Genetic Code: A Combinatorial and Atomic Analysis*), I highlighted multi-scale numerical invariants within the genetic code. These invariants reappear — with remarkable elegance — in the application of the first distributive law used in electrical circuits, as taught by Angelo C. Gillie.

From this observation, I sought to go further and examine whether codons could be paralleled with binary arithmetic and Boolean algebra. Boolean functions can indeed be related not only to the DNA strands, but also to gene activation and inhibition functions (ON/OFF), Venn diagrams, and all the possible combinations of a triplet.

This analogy extends to the second distributive law, and especially to universal truth tables, which represent all possible combinations of states 0 and 1 within a closed system. As will be shown below, the genetic code $(TCAG)^3$ fits perfectly within a complete Boolean structure, identical to that used in mathematical logic or electronic circuit theory.

“Universe Tables” for Two, Three, Four, and Six Variables (6 Bits)

These *universe tables* represent the exhaustive logical space of all possible binary combinations for a given number of variables — exactly as used in digital logic, switching theory, and Boolean algebra.

- For two variables (2 bits) → 2^2 = 4 possible states
- For three variables (3 bits) → 2^3 = 8 possible states
- For four variables (4 bits) → 2^4 = 16 possible states

- For six variables (6 bits) $\rightarrow 2^6$ = 64 possible states

This last configuration — the six-variable (6-bit) system — corresponds precisely to the genetic code, composed of 64 codons. Each codon can thus be interpreted as a unique logical state within the Boolean universe, making the genetic code a biological instantiation of a complete 6-bit Boolean space.

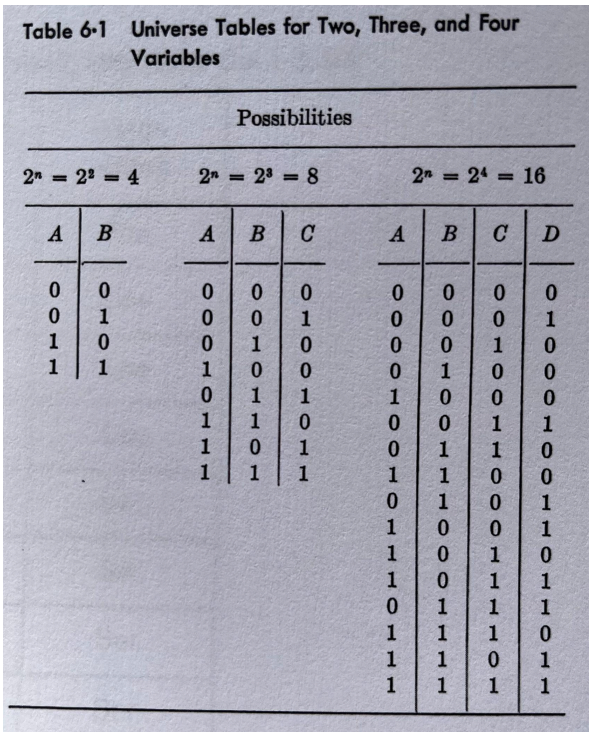


Table 6·1 Universe Tables for Two, Three, and Four Variables

Possibilities

$2^n = 2^2 = 4$

A	B
0	0
0	1
1	0
1	1

$2^n = 2^3 = 8$

A	B	C
0	0	0
0	0	1
0	1	0
1	0	0
0	1	1
1	1	0
1	0	1
1	1	1

$2^n = 2^4 = 16$

A	B	C	D
0	0	0	0
0	0	0	1
0	0	1	0
0	1	0	0
1	0	0	0
0	0	1	1
0	1	1	0
1	1	0	0
0	1	0	1
1	0	0	1
1	0	1	0
1	0	1	1
0	1	1	1
1	1	1	0
1	1	0	1
1	1	1	1

Table 6-1 d'Angelo C. Gillie page 96.

(TCAG³ → 6 bits), indexed from 1 to 64
(based on my calculations derived from the previous tables of C. Gillie),
representing a **complete Boolean structure**.

#	A	B	C	D	E	F	Codon	Amino acids
1	0	0	0	0	0	0	TTT	Phe
2	0	0	0	0	0	1	TTC	Phe
3	0	0	0	0	1	0	TTA	Leu
4	0	0	0	0	1	1	TTG	Leu
5	0	0	0	1	0	0	TCT	Ser
6	0	0	0	1	0	1	TCC	Ser

7	0	0	0	1	1	0	TCA	Ser
8	0	0	0	1	1	1	TCG	Ser
9	0	0	1	0	0	0	TAT	Tyr
10	0	0	1	0	0	1	TAC	Tyr
11	0	0	1	0	1	0	TAA	Stop
12	0	0	1	0	1	1	TAG	Stop
13	0	0	1	1	0	0	TGT	Cys
14	0	0	1	1	0	1	TGC	Cys
15	0	0	1	1	1	0	TGA	Stop
16	0	0	1	1	1	1	TGG	Trp
17	0	1	0	0	0	0	CTT	Leu
18	0	1	0	0	0	1	CTC	Leu
19	0	1	0	0	1	0	CTA	Leu
20	0	1	0	0	1	1	CTG	Leu
21	0	1	0	1	0	0	CCT	Pro
22	0	1	0	1	0	1	CCC	Pro
23	0	1	0	1	1	0	CCA	Pro
24	0	1	0	1	1	1	CCG	Pro
25	0	1	1	0	0	0	CAT	His
26	0	1	1	0	0	1	CAC	His
27	0	1	1	0	1	0	CAA	Gln
28	0	1	1	0	1	1	CAG	Gln
29	0	1	1	1	0	0	CGT	Arg
30	0	1	1	1	0	1	CGC	Arg
31	0	1	1	1	1	0	CGA	Arg
32	0	1	1	1	1	1	CGG	Arg

33	1	0	0	0	0	0	ATT	Ile
34	1	0	0	0	0	1	ATC	Ile
35	1	0	0	0	1	0	ATA	Ile
36	1	0	0	0	1	1	ATG	Met
37	1	0	0	1	0	0	ACT	Thr
38	1	0	0	1	0	1	ACC	Thr
39	1	0	0	1	1	0	ACA	Thr
40	1	0	0	1	1	1	ACG	Thr
41	1	0	1	0	0	0	AAT	Asn
42	1	0	1	0	0	1	AAC	Asn
43	1	0	1	0	1	0	AAA	Lys
44	1	0	1	0	1	1	AAG	Lys
45	1	0	1	1	0	0	AGT	Ser
46	1	0	1	1	0	1	AGC	Ser
47	1	0	1	1	1	0	AGA	Arg
48	1	0	1	1	1	1	AGG	Arg
49	1	1	0	0	0	0	GTT	Val
50	1	1	0	0	0	1	GTC	Val
51	1	1	0	0	1	0	GTA	Val
52	1	1	0	0	1	1	GTG	Val
53	1	1	0	1	0	0	GCT	Ala
54	1	1	0	1	0	1	GCC	Ala
55	1	1	0	1	1	0	GCA	Ala
56	1	1	0	1	1	1	GCG	Ala
57	1	1	1	0	0	0	GAT	Asp
58	1	1	1	0	0	1	GAC	Asp

59	1	1	1	0	1	0	GAA	Glu
60	1	1	1	0	1	1	GAG	Glu
61	1	1	1	1	0	0	GGT	Gly
62	1	1	1	1	0	1	GGC	Gly
63	1	1	1	1	1	0	GGA	Gly
64	1	1	1	1	1	1	GGG	Gly

Level 2^3: Logical Hinge Between the Base and the Doublet

In the universal truth tables derived from Boolean algebra, each power of two corresponds to an increase in the system's logical degree of freedom.

Thus, 2^2 represents a set of four fundamental states, which can be associated with the four nucleotidic bases (T, C, A, G) or, at a more elementary level, with the four principal atoms of life (C, H, O, N). The next level, 2^4 , corresponds to the nucleotide doublets described by Crick in his pre-code hypothesis, where two successive positions already structure a logical redundancy.

Between these two scales lies a rarely explored intermediate level: $2^3 = 8.$ This intermediate level carries a particular combinatorial and biophysical significance, as it represents the first closed form of the binary system with three variables — that is, the smallest logical space capable of self-coherence. In a three-bit system, eight combinations are possible: this is the **first complete hypercube (binary cube)**, which will later serve as the geometric foundation for the triplet structure $(TCAG)^3$ of the genetic code. One may thus regard this level as the logical skeleton of the future three-position code.

At the biochemical level, $2^3 = 8$ could correspond to configurations of interactions between bases — notably the possible combinations of hydrogen bonds (strong/weak, donor/acceptor) or the electronic polarity states within nucleotide pairs. These eight states would define a physical pre-organization of the code, a level of logical structuring preceding the stable formation of doublets.

At the informational level, the eight-state system constitutes a minimal encoding unit — a primitive biological byte. It represents the first level at which living matter can be described in terms of logical self-reference: the system is both closed (all possible combinations are present) and extensible (each combination can serve as a foundation for higher-order structures).

Thus, the progression

$$4 \rightarrow 8 \rightarrow 16 \rightarrow 64$$

reflects the rising complexity of life's logic, from the elementary alphabet of the bases to the complete combinatorial structure of the codons.

This level 2^3 acts as a mathematical and physical hinge: it links the atomic stability of life (level 4) to the informational dynamics of the code (level 16 and beyond), marking the transition point where logic becomes geometry — that of the binary cube, the direct precursor of the invariant sphere of the genetic code.

In summary:

Level	Structure	Biological Interpretation	Logical Interpretation
$2^2 = 4$	Bases / Atoms	Fundamental alphabet	Binary variables
$2^3 = 8$	Logical pre-code	Binary states of pairs / H-bond configurations	Minimal biological byte
$2^4 = 16$	Doublets (Crick)	Pre-codons / dinucleotides	Ordered combinatorial structure
$2^6 = 64$	Triplets (codons)	Complete genetic code	6D Boolean hypercube

Where Logic Becomes Geometry: Representation of the Genetic Code as a Boolean Cube $(TCAG)^3$

The following diagram shows the three-dimensional projection of a six-dimensional logical cube ($2^6 = 64$ vertices), representing the complete combinatorial space of the genetic code. Each axis symbolizes one of the three positions of the codon, labeled Position 1, Position 2, and Position 3.

On each axis, the four bases (T, C, A, G) are represented as equidistant nodes, encoded by their binary values:

T = 00
C = 01
A = 10
G = 11

The combination $(TCAG)^3$ generates 64 vertices, each corresponding to a unique codon. These vertices form a binary hypercube, whose 3D projection reveals zones of symmetry and redundancy—mirroring the structure of the biological codon table.

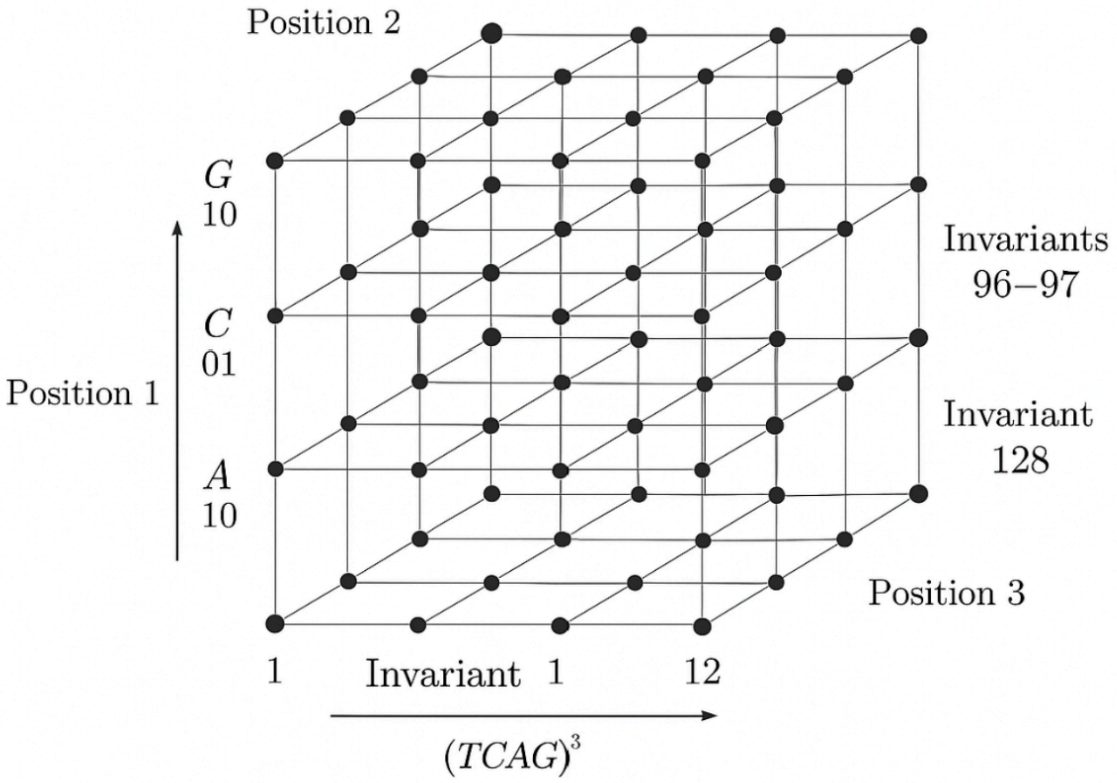
Annotations:

The central region is labeled “Invariant 1”, corresponding to the fundamental logical state (origin).

Two lateral zones, separated by a transition boundary, are labeled “Invariants 96–97”, representing the internal discontinuity between symmetrical subcubes of the system.

The outer perimeter is marked “Invariant 128”, indicating the saturation threshold of the system.

The logical cube $(TCAG)^3$ illustrates the exact correspondence between the 6-bit Boolean combinatorial structure and the genetic code: each codon can be identified by its specific position within this space. The numerical invariants describe the stability and transition of logical states within the complete system.



The constant Δ = 225.5 — the sum of all invariants — can also be added, as discussed in the second part of this research (*Multiscale Numerical Invariants and Fractal Properties of the Genetic Code: Internal Constraints and Multiscale Packet Distributions Revealing a Universal Grammar.* Zenodo. https://doi.org/10.5281/zenodo.17272500).

This constant represents the global equilibrium point of the system, integrating the local invariants (1, 96–97, 128) into a single numerical signature. It expresses the closure and coherence of the genetic code as a complete logical manifold, where atomic, combinatorial, and informational levels converge into a unified grammar of life.

Dimensional Correspondence Between the Genetic Cube and the Boolean Hypercube

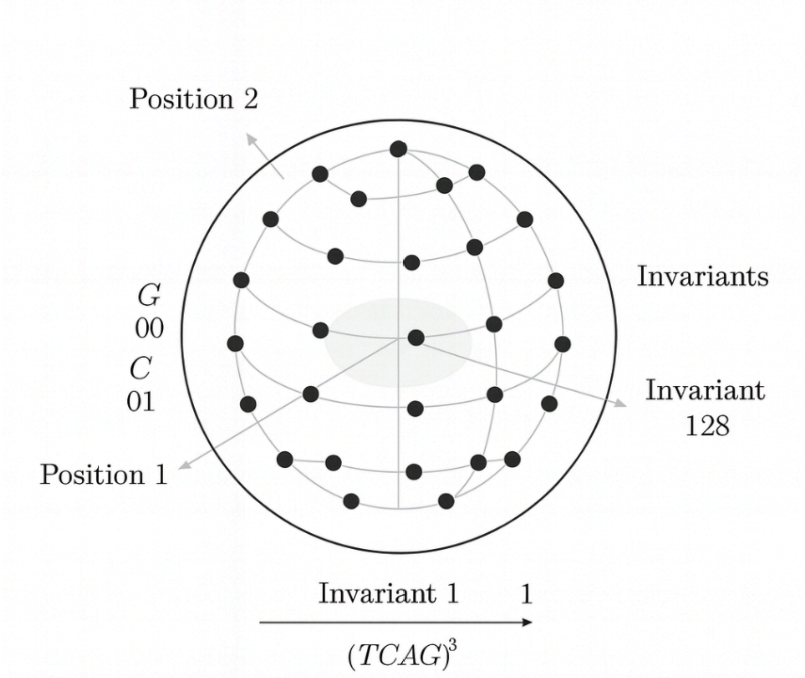
Although the genetic code (TCAG)³ is generally represented as a three-dimensional cube — each axis corresponding to one codon position — this visualization is merely a projection of a higher-dimensional logical structure. Each codon position can assume four possible states (T, C, A, G), and since four states can be encoded by two binary bits (00, 01, 10, 11), the triplet configuration in fact corresponds to six independent binary variables (2 bits × 3 positions).

Formally, the complete set of codons $^{64\ \text{codons}\ (4^3)}$ is therefore equivalent to a six-dimensional Boolean hypercube $^{(2^6)}$. In this representation, each vertex of the hypercube corresponds to a unique codon, and each edge represents an elementary binary transition (mutation or logical change) between two codons differing by a single bit.

The three-dimensional “genetic cube” commonly used in biological representations is thus only a topological projection of this six-dimensional logical space — one that preserves neighborhood relationships and combinatorial symmetry, while simplifying dimensional complexity for visualization purposes.

This equivalence demonstrates that the genetic code is quaternary in its biological expression yet binary in its logical foundation, and that the transformation $(TCAG)^3 \rightarrow 2^6$ from one to the other is not merely symbolic but structurally exact. It also explains the emergence of the numerical invariants resulting from the cubing of the code, as these invariants arise naturally from the internal geometry of the Boolean hypercube rather than from any empirical adjustment.

Spherical Projection and Correspondence with the Bloch Sphere



The geometric projection of the invariant system $(TCAG)^3$ onto a spherical surface reveals a direct parallel with the quantum formalism of the Bloch sphere. In quantum mechanics, the Bloch sphere represents the set of all possible states of a two-level system (|0⟩, |1⟩), where each point on the sphere corresponds to a distinct superposition of basis states.

Analogously, the biological system composed of the four nucleotides (T, C, A, G), organized in triplets, can be described as a discrete extension of this model, encompassing $4^3 = 64$ combinatorial states. Each point on the sphere of invariants thus corresponds to a codon — that is, a unique logical configuration derived from a six-bit Boolean cube (2^6) projected into a normalized three-dimensional space.

This projection transforms the discrete combinatorial structure of the cube into a continuous topological surface, preserving the intrinsic symmetries of the code while revealing its quantum-like organization.

The resulting spherical representation exhibits the same mathematical properties as electronic orbitals — symmetry, quantization, and directional degeneracy — where each codon occupies a defined position on the sphere, analogous to a localized probability amplitude ($|\psi|^2 = 1$).

The invariants (1, 96–97, 128) define quantized layers within this spherical structure:

- Invariant 1 marks the fundamental logical state, equivalent to the origin of the Bloch sphere;
- Invariants 96–97 delineate an intermediate zone of degeneracy, analogous to spin coupling or the doubling of p orbitals;
- Invariant 128 defines the outer boundary, corresponding to the saturation of the combinatorial space (2^7).

Thus, the sphere of invariants functions as a biological analogue of the Bloch sphere, representing the totality of possible codonic states within a normalized geometric field. This correspondence extends the notion of quantization — from the electron in its orbital to the codon within the genome — and suggests that atomic and genetic architectures obey the same fundamental law of discrete symmetry, inscribed within a continuous probabilistic geometry.

Mathematical Appendix: Projection of the Boolean Cube onto a Normalized Sphere

Consider a combinatorial system of *n* binary variables, defining a **logical hypercube** of dimension *n* with 2^n vertices. Each vertex can be represented by a binary vector

$$\mathbf{v_i} = (x_1, x_2, ..., x_n), \quad \text{where } x_k \in \{0, 1\}$$

For the biological system $(TCAG)^3$, each base is represented by two bits (00, 01, 10, 11), thus forming a **six-dimensional cube (n = 6)** containing **64 distinct states**.

The **spherical projection** of this hypercube into a three-dimensional space (x,y,z) is obtained by normalizing the binary coordinates:

$$\begin{cases} x = \sin(\theta)\cos(\phi) \\ y = \sin(\theta)\sin(\phi) \\ z = \cos(\theta) \end{cases} \quad \text{where } \theta, \phi \in [0, \pi]$$

Each pair (θ_i, ϕ_i) corresponds to a unique codon, projected from the logical cube onto the sphere of invariants.

The normalization condition imposes:

$$x^2 + y^2 + z^2 = 1$$

which ensures that all codonic states are distributed over the surface of a unit sphere, analogous to the Bloch sphere in quantum mechanics.

Within this framework, the numerical invariants define discrete radial layers:

$$r_1 = 1, \quad r_{96\text{–}97} \approx \sqrt{\frac{3}{4}}, \quad r_{128} = 1$$

where r_i designates the normalized radius associated with each domain of invariance. These layers represent zones of combinatorial stability, comparable to electronic energy levels (s, p, d, f) in atomic orbitals.

Finally, the probabilistic interpretation naturally derives from the logical occupancy density:

$$P_i = |\psi_i|^2 = \frac{1}{64}$$

each codon having the same probability of occurrence on the normalized sphere under a neutral state (absence of selective bias).

Local deformations of this density (accumulations, ruptures at 9 or 96–97) thus correspond to symmetry breakings equivalent to electronic transitions observed in real orbitals.

Complementary Appendix: Correspondence Between Hilbert Space and Codon Combinatorics

In quantum formalism, any two-level system — denoted $|0\rangle$ and $|1\rangle$ — can be described as a state vector in a Hilbert space of dimension 2.

A linear combination of these states defines a **quantum superposition**:

$$|\psi\rangle = \alpha|0\rangle + \beta|1\rangle, \quad \text{where } |\alpha|^2 + |\beta|^2 = 1$$

Analogously, a biological base (T, C, A, G) can be represented as a logical superposition of two bits, forming four distinct states:

$$T = |00\rangle, \quad C = |01\rangle, \quad A = |10\rangle, \quad G = |11\rangle$$

Thus, the triplet $(TCAG)^3$ corresponds to a **three-qubit system**, or more precisely, to a tensor product of Hilbert spaces:

$$\mathcal{H}_{\text{codon}} = \mathcal{H}_2 \otimes \mathcal{H}_2 \otimes \mathcal{H}_2 = \mathcal{H}_8$$

Since each base contains two bits, the entire set of 64 codons forms an **equivalent 6-qubit space**:

$$\mathcal{H}_{\text{genome local}} = \mathcal{H}_2^{\otimes 6}$$

that is, the same 64-dimensional vector space used to describe a quantum system with six binary degrees of freedom.

Within this combinatorial space:

- Logical operations on codons (transitions, inversions, substitutions) play the role of unitary operators UUU acting on Hilbert states;
- The numerical invariants (1, 96–97, 128) correspond to the stable eigenvalues of these transformations;
- The spherical projection (x,y,z) represents the normalization of the global quantum state, analogous to the Bloch sphere for an individual qubit.

Thus, the genetic code can be interpreted as a discrete Hilbert space, in which codons behave as quantified states of biological information. This correspondence suggests that the combinatorial logic observed in genomic structure stems from a formal unification principle between information physics and molecular biology: **Each codon is a discrete projection of a global information state, analogous to a quantum state vector in a normalized space**.

Hypothesis of Biological Superposition: Quantized Continuity of Life Within the Combinatorial Space of the Genetic Code

The combinatorial analysis of the genetic code $(TCAG)^3$, considered as a six-dimensional Boolean hypercube projected onto a normalized sphere, suggests that all forms of life share a common informational structure, mathematically equivalent to a quantized state space.

Each codon corresponds to a state vector $|\psi_i\rangle$ in a discrete Hilbert space $\mathcal{H}_2^{\otimes 6}$, forming the basis of all possible biological combinations.

In this representation, living organisms do not constitute independent entities but rather temporal and spatial superpositions of logical configurations of the same fundamental code. Thus, the biological diversity observed — whether molecular, ecological, or evolutionary — can be interpreted as a dynamic distribution of states within this global combinatorial field. Each form of life represents a localized projection of a universal biological state function, analogous to the collapse of the wave function in a quantum system. Phenomena such as emergence, mutation, and extinction then correspond to informational phase transitions, without rupture of the overarching logical framework.

The numerical invariants (1, 96–97, 128), identified as structural constants of the system, define stability thresholds within this combinatorial space:

- Invariant 1 corresponds to the fundamental coherence state of the code;
- Invariants 96–97 mark the transition zone between stable subspaces;
- Invariant 128 delineates the maximum extension threshold of the system (2^7).

These values, consistent with the progression of electronic orbitals and the symmetry properties of the Bloch sphere, suggest that life obeys the same laws of quantization and normalization as matter itself. In other words, biological, atomic, and logical structures all derive from a common principle of information conservation, expressed across different scales.

This hypothesis of biological superposition invites us to consider all forms of life — past, present, and future — as quantized facets of a single universal informational system. Each organism would represent a stable configuration within a global space of possibilities, locally expressing a portion of the total coherence of life.

Combinatorial Hierarchy and the Potential Infinity of the Living Code

The genetic code, based on four bases (T, C, A, G) organized in triplets, defines a finite system of 64 elementary combinations.

These 64 codons constitute the complete logical basis of life: a closed Boolean space (2^6), corresponding to the combinatorial sphere of invariants previously described. This system, though finite, possesses the fundamental property of being combinatorially extensible: it serves as a stable foundation for a set of potentially infinite structures.

1. From Codons to Amino Acids: Projection of the Discrete Code

Each codon encodes one of the 20 canonical amino acids, with redundancies that ensure the robustness of translation.

Thus, the passage from the codonic level (64 states) to the proteic level (20 functional states) constitutes a projection from a six-dimensional logical space to a reduced but biochemically operational dimension.

This reduction does not eliminate combinatorial richness — it channels it.

If we consider a protein of 100 amino acids, the number of possible sequences is on the order of:

$$N_{\text{proteic}} = 20^{100} \approx 1.27 \times 10^{130}$$

For a protein of 300 amino acids, typical of the human genome, we obtain:

$$N_{\text{proteic}} = 20^{300} \approx 10^{390}$$

a number exceeding by several orders of magnitude the total number of atoms in the observable universe 10^{80}.

Thus, a finite alphabet (64 codons, 20 amino acids) generates a quasi-infinite continuum of combinations. This phenomenon illustrates **the fundamental property of the genetic code: it is discrete in its basis, yet unlimited in its realizations.**

2. From Proteins to Genes: Emergence of Hierarchical Complexity

Proteins then associate into functional modules (enzymatic complexes, receptors, cytoplasmic structures), which integrate into networks of genetic and metabolic regulation. At the genomic scale, humans possess about 20,000 genes, but the combinatorics of their interactions (exons, introns, regulators, isoforms) lead to millions of possible expression states.

If we consider the possible codon combinations for an average gene of 1,000 bases (i.e., 333 codons), the number of theoretical arrangements is:

$$N_{\text{gene}} = 64^{333} \approx 10^{600}$$

In other words, from a logical space of 64 symbols, **biology generates a state space exceeding all known computational limits**.

3. Finite System, Infinite Potential

This apparent paradox — a finite system capable of producing an infinity of states — is the hallmark of fractal and self-similar structures. Within this framework, the genetic code behaves as an orthonormal basis of the state space of life, analogous to the basis of a discrete Hilbert space. Amino acids and proteins thus correspond to superpositions of these base states, that is, to vectorial combinations within a very high-dimensional space. Each living organism represents a coherent projection of this global combinatorial field.

The living code follows a general law:

$$\text{Biological diversity} = f(\text{hierarchy of combinations}) \quad \text{with} \quad f(x) \to \infty.$$

This equation expresses the **universal property of the system**: A finite set of Boolean rules generates an infinity of stable configurations across the scales of life.

4. Consequence: Life as an Information-Expanding System

The combinatorial hierarchy of the genetic code explains both the stability of life (ensured by the invariants) and its unlimited creativity (made possible by the combinatorics of higher levels). The code is not a closed dictionary, but rather a state generator, whose manifestations emerge progressively according to environmental and temporal constraints.

Thus, biological evolution can be understood not as a succession of random mutations, but as a structured exploration of the combinatorial space of the living code — a space whose size, though founded on a finite alphabet, tends toward infinity in its functional potentialities.

In this sense, life is not the product of chance, but the progressive development of a finite logical system toward its maximal space of expression.

Correspondence Between the Mirror-Twin Theory and the Combinatorial Structure of the Genetic Code

The Mirror-Twin Theory (Kayser, 2024, *The Mirror-Twin Paradox: A New Approach to DNA*) naturally integrates within the combinatorial and spherical model of the genetic code. In this framework, the inversion of bases — or mirror transformation of the code — is not a mere permutation operation but an intrinsic symmetry of the state space defined by the Boolean cube and its spherical projection. Each inversion represents a geometric transformation valid within the internal symmetry group of this space: it performs a vector reflection across a plane of invariance, generating a topological correspondence between two complementary regions of the system.

The experimentally observed correspondences between inverted sequences and real sequences thus find their geometric justification: they express the partial stability of the invariants (1, 96–97, 128) under mirror inversion. In other words, these invariants act as fixed points or coherence anchors within the combinatorial space of the code; they remain unchanged when the system undergoes inversion of its binary coordinates. The mirror twins therefore appear as conjugate state pairs — two symmetrical manifestations of the same informational configuration — analogous to conjugate spin states on the Bloch sphere.

This property confirms that mirror symmetry is not an anomaly of the code, but a direct consequence of its complete Boolean structure and normalized spherical projection. The existence of these informational twins strengthens the hypothesis of a unified combinatorial field of life, in which each biological form may possess a conjugate or mirror state, defined by the internal geometry of the code rather than by its molecular expression.

Thus, the Mirror-Twin Theory constitutes a natural extension of the invariant model: it illustrates the logical reversibility of the genetic code and suggests the existence of a fundamental symmetry of life, comparable to that of conjugate quantum states.

Transmission of Biological Information: The Continuity of State Within the Code

The replication of the genetic code, traditionally described as a chemical process of molecular duplication, can be reinterpreted as a continuity of state phenomenon within a quantized informational space.

Within the Boolean model $(TCAG)^3$, each codon corresponds to a logical state vector $|\psi_i\rangle$ in a discrete Hilbert space composed of 64 elementary configurations. The entire genome can thus be viewed as a structured superposition of these states — a coherent information function inscribed within the combinatorial sphere of life.

The transmission of DNA from one generation to the next therefore does not represent a simple material copy, but rather the reinstantiation of a stable configuration within the same state space. Each replication or reproductive cycle corresponds to a reactualization of the code — a renewed yet topologically equivalent projection of the same informational function. Hence, it is not the molecule as an object that perpetuates itself, but the logical coherence of the system, preserved through its chemical and temporal transformations.

In this perspective, biological reproduction can be understood as a phase maintenance process within a self-coherent informational field: each living organism is merely a quantized state of this field, a temporarily stable solution to the combinatorial equation of life. During replication, the logical phase of information is conserved, ensuring the continuity of the code beyond molecular variability. Heredity thus becomes the direct consequence of the conservation of informational state, rather than merely the chemical fidelity of nucleotides.

The invariants (1, 96–97, 128), identified as stability anchors across all scales of the system, play a fundamental role here: they ensure the topological stability of the combinatorial field, preventing any rupture of coherence during replication cycles. These constants define the stable phase zones of the code, analogous to electronic orbitals preserving their quantum numbers despite energy transitions.

Thus, genetic transmission can be reformulated as an emergent property of the logical continuity of the code. Biological information reproduces itself not through chemical inertia, but through the persistence of an invariant logical state, manifesting successively through different material structures.

In this interpretation, life does not perpetuate itself through mere molecular reproduction: it persists as a self-coherent informational wave, resonating through time and generations, continuously reactivating the same universal quantum state of living matter.

Origin of Biological Information: From Logical Field to Matter

The origin of biological information cannot be understood solely through the chemical mechanisms of replication or mutation. Within the framework of the combinatorial model $(TCAG)^3$, information precedes matter: it does not arise from material processes but corresponds to the fundamental logical structure that makes all material organization possible.

The Boolean system defines, for each number of variables, a finite yet complete space of combinations governed by laws of symmetry and invariance. This space constitutes a field of logical order — a set of mathematical constraints independent of any physical substrate. The "primary information" thus resides in the topology of the possible itself: it describes how discrete states can combine without internal contradiction. When matter appears, it does not create this information; rather, it becomes its coherent carrier, allowing the logical structure to manifest in dynamic form.

Within this framework, the origin of life corresponds to the moment when a stable molecular substrate — composed of CHON atoms capable of self-association and replication — enabled the materialization of a subset of the universal logical field. The first self-replicating structures therefore did not generate biological information; they represented its first stable instantiation. They mark the transition from an abstract informational field to a physicochemical realization compatible with the constraints of Boolean coherence.

This process can be described as a progressive symmetrization of reality: pure logic, defined by the possible states of the system, projects itself into a material space capable of sustaining it. Life does not emerge as an isolated event, but as the actualization of a pre-existing configuration of information. In other words, the genetic code was not "invented" by biology — it was revealed when matter reached the necessary level of complexity to align with its logical structure.

This hypothesis leads to a reformulation of the concept of the "origin of life": life does not arise from inert matter, but from the convergence between a stable informational topology and a chemical resonance capable of ensuring its persistence. Biological matter thus becomes the local realization of a universal combinatorial law.

The invariants (1, 96–97, 128) play, in this context, the role of cosmological structuring constants. Across atomic, molecular, and biological scales, they express the same requirement of numerical and geometric coherence. Their recurrence suggests that the logic of life is not contingent, but derives from a universal principle of information organization.

Thus, biological information has no historical origin: it is ontologically prior to matter, and biology is merely one of its manifestations. DNA, proteins, and cellular networks represent distinct material expressions of the same invariant logical field, whose fundamental function is the preservation of coherence through time, transformation, and reproduction.

Consequences and Perspectives: Toward a Biology of Informational Coherence

If biological information precedes matter, and if the genetic code represents the projection of an invariant logical space, then biology can be redefined as the science of coherent states of

information within matter. The evolution of life would no longer be seen as the outcome of random mutations and selections, but rather as the result of state transitions within an informational field striving to maintain internal coherence despite the variability of its material substrates.

This approach opens the way to a biology of informational resonance, in which each organism represents a local solution of a universal combinatorial system. Evolutionary transformations would correspond to phase transitions within this field, analogous to state transitions in quantum physics, where symmetry breakings give rise to new stable configurations. In this context, the diversification of life reflects a topological exploration of configurations permitted by the code, rather than a succession of random contingencies.

Such a framework also renews the question of the origin of life. If the logical structure of the code exists independently of its substrate, then life could emerge whenever matter reaches the threshold of complexity required to align with the constraints of the informational field.

This conception renders biology fundamentally universal: it implies that different forms of life — on Earth or elsewhere — could manifest the same logical architecture under diverse chemical or physical expressions. Thus, exobiology need not search for life *as we know it*, but rather for coherent structures capable of encoding and preserving information according to the same principles of symmetry and invariance.

Finally, understanding living systems as expressions of informational coherence could illuminate aspects of biological consciousness. If organisms are projections of a global logical field, then consciousness — in the broad sense — may emerge as a resonant property between the different levels of the code: molecular, cellular, neuronal, and collective. It would not be an isolated phenomenon, but a reflexive expression of the code upon itself — the ability of a living system to perceive itself as a particular state within a universal informational field.

In summary, this framework unifies three domains that have traditionally remained separate:

- Molecular biology, which describes the material carriers of information;
- Quantum physics, which formalizes the logic of states and transitions;
- Philosophy of information, which questions the nature and permanence of informational structures.

It opens the perspective of a post-materialist biology, founded not on substance but on the coherence of states. Within this paradigm, life, evolution, and consciousness emerge as local manifestations of a single law of information conservation, expressed through varying degrees of complexity.

Thus, life would not be the product of chemical chance, but rather the form that coherence takes when it becomes inscribed within matter.

Informational Expansion of Life: Cosmological Analogy of the Genetic Code

When viewed through the lens of Boolean combinatorics $(TCAG)^3$, the genetic code exhibits mathematical properties analogous to those observed in physical cosmology. Just as the universe expands from an initial state dense in energy and information, the living code unfolds from a minimal combinatorial state toward an ever-expanding informational space, governed by a set of stable numerical invariants.

1. Logical Singularity and Combinatorial Expansion

The initial state of the code — defined by four bases and three positions ($4^3 = 64\ \text{combinations}$)— represents a logical singularity, a point of origin from which all biological structures can emerge.
This defined base generates an exponential unfolding of possibilities:

$$64 \ \Rightarrow \ 20 \ \Rightarrow \ 10^{390}\ (\text{proteins}) \ \Rightarrow \ 10^{600+}\ (\text{genes and interactions})$$

- From 64 codons, the system produces 20 amino acids and multiple folding patterns, giving rise to proteins, genes, and ultimately entire organisms.
- Each new level of organization (molecular → cellular → organismal → ecological) corresponds to a higher-order projection of the same combinatorial foundation.
- The invariants (1, 96–97, 128) play the role of cosmological constants of life, preserving the coherence of the expansion as new informational “layers” appear.

Thus, the combinatorial space of the code behaves like a living universe of information, where each new structure is not an addition but a reconfiguration of existing logical relationships — analogous to the cosmological inflation that expands the fabric of spacetime without altering its underlying geometry.

2. Conservation of Invariants and Stability of the Field

The informational expansion of life unfolds without altering its fundamental laws. The numerical invariants (1, 96–97, 128) identified within the structure of the code fulfill a role analogous to that of cosmological constants in the physical universe: they govern the stability of the expansion field.

- Invariant 1 — corresponds to the initial state of absolute coherence, the *logical singularity* from which the entire system emerges.
- Invariants 96–97 — mark a state transition between two regimes of organization, analogous to matter–radiation decoupling in standard cosmology.
- Invariant 128 — sets a structural boundary for the local expansion of the combinatorial field, the biological equivalent of an observable horizon.

Thus, the dynamics of the code follow a principle of coherence conservation, analogous to the conservation of energy in the universe: the diversity of forms never alters the fundamental structure of the informational field.

3. Non-Entropic Expansion: Growth of Coherence

Unlike the material universe, whose expansion is accompanied by an increase in entropy, the expansion of the living code produces an increase in coherence. Each new combination does not introduce disorder but instead reveals a latent order already embedded within the original structure.

This property distinguishes biology from the rest of physics: it is founded upon a principle of informational self-organization, rather than energetic dispersion.

In other words:

$$\text{Physical expansion} \Rightarrow \text{dilution of energy density}, \quad \text{Biological expansion} \Rightarrow \text{densification of logical coherence}.$$

4. Fractal Structure and Scale Continuity

Just as the universe develops hierarchical structures (particles → atoms → galaxies → clusters), living systems exhibit a parallel hierarchy (bases → codons → proteins → genes → organisms). In both cases, the same fractal geometry of expansion emerges: each level encodes the laws of the previous one while introducing a higher degree of freedom.

This self-similarity suggests that the universe and life share a common informational grammar, expressed at different scales of organization. Hence, biology appears as a specific instance of an informational cosmology, in which living matter constitutes a condensed phase of the universal logical field.

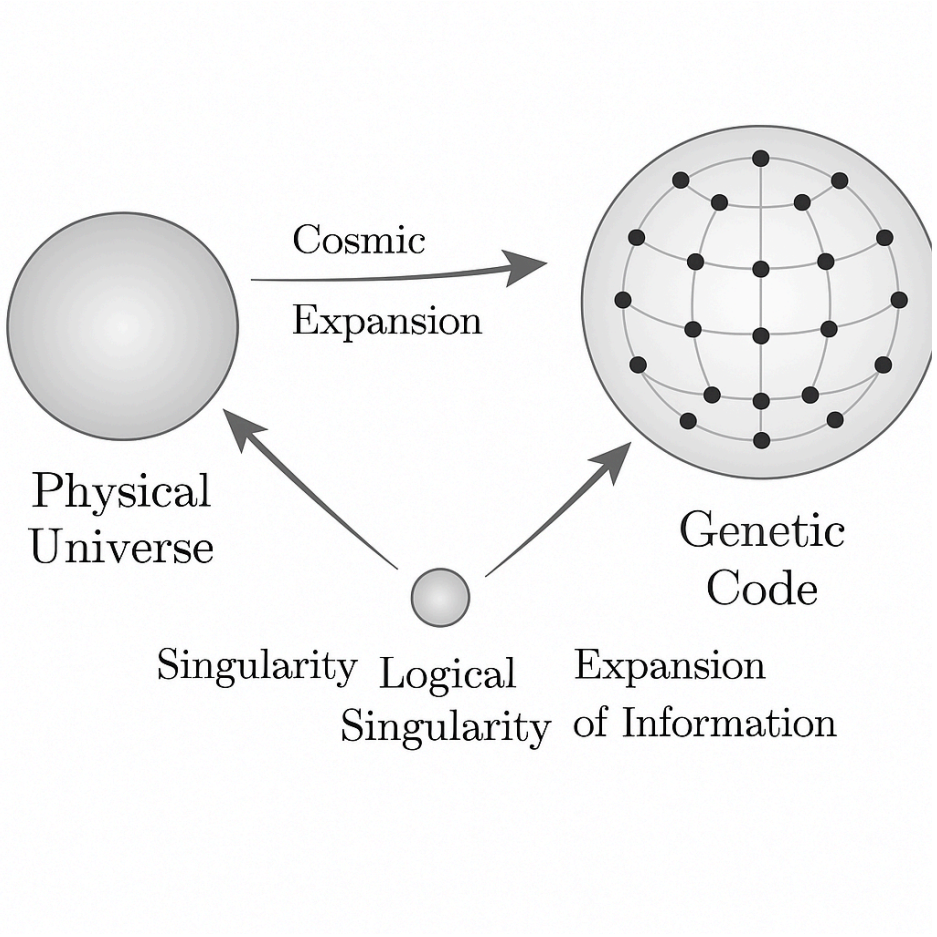
The genetic code, far from being a biological exception, represents the embodied version of a fundamental cosmological principle: the natural tendency of information to structure, reproduce, and expand while preserving its invariants.

5. Synthesis: Informational Expansion of Life

This analogy between **cosmic expansion** and **biological expansion** leads to a unified reformulation: **The universe and life are two expressions of the same process of informational expansion.** In both cases, a finite set of initial laws generates a continuously growing space, regulated by stable invariants.

The **universe expands within the field of matter**, while **life expands within the field of coherence**. Biological invariants play the role of constants of informational expansion, maintaining the logical order of living systems within their infinite development.

Thus, biology can be understood as the internal cosmology of matter — the manifestation, at the scale of life, of the very same principle of expansion that governs the universe as a whole.



Boolean Matrices

As mentioned in the third part of my research (*Multiscale Numerical Invariants and Fractal Properties of the Genetic Code: Internal Constraints and Multiscale Packet Distributions Revealing a Universal Grammar*), a foundational matrix was generated from the identified numerical invariants.

This matrix constitutes a minimal fractal basis, enabling the representation of the fundamental building blocks from which the system's structure emerges, and allowing for predictive modeling of hypothetical, higher-order genetic codes.

$$\mathbf{b} = \begin{bmatrix} 602.5 \\ 828 \\ 1205 \\ 1430.5 \\ 1656 \\ 1807 \\ 2033 \\ 2258 \\ 2484 \end{bmatrix} \in \mathbb{R}^9$$

This vector represents the minimal fractal basis —
the set of fundamental “blocks” from which the system’s structure emerges.

From this foundation, I explored the possibility of applying these regularities to Boolean algebra, in order to examine how such a numerical structure might correspond to a discrete logical system. Unsurprisingly, the codon table integrates naturally with the fundamental principles of binary logic described in Angelo C. Gillie’s manual, particularly in the sections on switching circuit simplification techniques (p. 109), Boolean matrices (chap. 7), and unsimplified node circuit matrices (p. 123).

The correspondences extend further to the Karnaugh maps (chap. 8), minimization of switches (p. 201), logic trees for pairs of flip-flops (p. 204), and odd parity-check state diagrams (p. 221).

Thus, it can be stated that the entire codon table fits seamlessly within the structure and laws of Boolean algebra, confirming the deep compatibility between the logic of life and the formal logic of electronic circuits.

Conclusion and Originality of the Proposed Framework

The analysis presented in this second part of *Meta-Genesis* demonstrates that the genetic code can be interpreted as a universal logical structure, organized according to the principles of Boolean algebra and binary arithmetic, whose numerical invariants (1, 96–97, 128) ensure the multiscale coherence of the biological system.

The cubing of the code appears as the mathematical condition for its completeness: it generates a six-dimensional hypercube (2^6 = 64 states), which constitutes the geometric foundation of the code and allows its spherical projection — an information state space comparable to the Bloch sphere in quantum physics.

Through this model, life ceases to be perceived as organized matter and instead becomes the geometric manifestation of a self-coherent logical field, capable of projecting itself across different combinatorial dimensions. The expansion of life, through the diversity of biological forms, thus corresponds to an expansion of informational coherence, analogous to the cosmic expansion of matter in the physical universe. The hierarchical levels of life — from nucleotide to cell, from organism to ecosystem — emerge as nested projections of a single

fundamental code, each biological form representing a local, temporarily stabilized solution of a global logical system.

Originality of the Conceptual Framework

This approach goes beyond the works of Rumer (1966), Sánchez & Grau (2004–2005), Nemzer (2016–2017), and Lenstra (2015), which described the genetic code as a combinatorial or symmetric system, yet confined to the canonical space of the 64 codons.

Here, the code is envisioned as a universal state function, capable of generating all manifestations of life from a single initial Boolean space.

For the first time, the genetic code is interpreted not only as a mathematical structure, but as a superposition of logical states — a quantified entity in which each living form corresponds to a distinct projection within the biological space-time continuum.

This interpretation introduces the notion of “quantum faces of a single code,” directly linking Boolean logic to the biophysics of information and the cosmology of life.

In this sense, *Meta-Genesis* proposes a shift in paradigm — from *descriptive* to *generative*, from *chemical* to *logical*, and from *biological* to *cosmological*.

The genetic code thus emerges as the mathematical signature of life: a universal language whose multiple projections generate the apparent diversity of living forms, while preserving the continuity of its underlying logical invariant.

Complete Primary Data, Computational Materials

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Suggested Complementary References

To situate the *Meta-Genesis* framework within a broader scientific, mathematical, and philosophical context, the following references are recommended. They cover key domains intersecting Boolean logic, theoretical biology, quantum information, and cosmology:

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